**Genotypic and Phenotypic Correlation Analysis of Morphological and Yield-Contributing Traits in Mustard (*Brassica juncea* L.) Genotypes Under Organic Conditions**

**Abstract**

The present study was undertaken to estimate the genotypic and phenotypic correlations among eleven morphological and yield-contributing traits in twelve mustard (Brassica juncea L.) genotypes grown under organic conditions at Bundelkhand University, Jhansi, during the rabi season of 2024–2025. Understanding these relationships is essential to improving selection efficiency for yield and its component traits. Strong and significant genotypic and phenotypic correlations were observed among several traits. Genotypic correlations were generally stronger than phenotypic ones, indicating a stronger inherent genetic relationship among traits beyond environmental influence. Seed yield per plant (SYP) was significantly and positively correlated at the genotypic level with number of seeds per siliqua (NSS), number of siliquae per plant (NSP), and biological yield (BY), indicating their importance as selection indices. Negative associations were also observed between plant height (PH) and total branches (NTB), suggesting trade-offs in trait selection. The study provides valuable insights for mustard breeders aiming to develop high-yielding varieties suitable for organic farming systems.

**Keywords**: Mustard genotypes, Correlation analysis, Genotypic association, Phenotypic traits, Yield components, Organic farming

1. **Introduction**

Mustard (*Brassica juncea* L.) is an important oilseed crop, and understanding the relationship between its various traits is crucial for effective breeding programs. With about 3500 species and 350 genera, the Brassicaceae family is one of the most commercially important plant groups (Warwick et al, 2000). Mustard or sarson as it is known in hindi has been mentioned in the Ayurvedic Samhitas. There are references to mustard seed in India from a story of Gautama Buddha in fifth century BC. Rapeseed-mustard, an oleiferous Brassica plant, is one of the most economically important agricultural commodities. The words rape and mustard are derived from the Latin word rapum, which means turnip, and the European habit of combining sweet must of old wine with crushed seeds of black mustard [B. nigra (L.) Koch] to make a heated paste. Since the fifteenth century, Europe has been growing mustard and rapeseed oilseeds. In the Indus Valley in 3000 BC, mustard seed and rapeseed were produced. From China, the Rai was brought to India. Mustard originated in eastern Europe and Cyberia. This study focuses on analyzing the genotypic and phenotypic correlations between different morphological and yield-contributing traits in mustard genotypes. Genotypic correlation reflects the inherent genetic relationship between traits, while phenotypic correlation includes both genetic and environmental influences. By examining these correlations, breeders can identify traits that are closely associated with yield and prioritize them for selection to improve overall productivity.

Mustard, or Brassica juncea, is a significant oilseed crop, particularly in India, where it contributes substantially to oil production. Breeding efforts aimed at enhancing yield rely heavily on understanding the genetic and phenotypic relationships among various traits. Analyzing these correlations helps identify which traits, when improved, will lead to a corresponding increase in seed yield.

Genotypic correlation, specifically, reveals the extent to which traits are linked due to their shared genes. For example, if two traits exhibit a strong positive genotypic correlation, it suggests that improving one trait is likely to positively influence the other, potentially leading to a synergistic effect on yield. Phenotypic correlation, on the other hand, encompasses both genetic and environmental influences on the relationship between traits. This provides a more realistic picture of how traits interact under field conditions.

Therefore, this study aims to determine both genotypic and phenotypic correlations between various morphological and yield-related traits in mustard genotypes. By understanding these relationships, breeders can make informed decisions about which traits to target in their breeding programs to maximize seed yield and overall productivity in mustard.

**2. Materials and Methods**

**2.1 Experimental Site**

The research trial was conducted during the rabi season of 2024–2025 at the Organic Research Farm, Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Bundelkhand University, Jhansi (U.P.), India. The site lies at a latitude of 26°44′ N and longitude of 79°25′ E with an elevation of 284 meters above mean sea level. It falls under Agro-Climatic Zone VIII (Central Plateau and Hill Region) and experiences a subtropical climate with cool winters and hot summers. The soil of the experimental field was sandy loam in texture, moderately fertile with good drainage, and maintained under organic management for the last five years.

**2.2 Plant Material and Experimental Design**

Twelve diverse genotypes of mustard (*Brassica juncea* L.) were selected for evaluation based on their morphological diversity and regional adaptability. The experiment was laid out in a Randomized Block Design (RBD) with three replications. Each plot consisted of three rows of 3 meters length with a row-to-row spacing of 30 cm and plant-to-plant spacing of 10 cm. Recommended organic cultivation practices were followed throughout the crop season. Nutrient requirements were met using farmyard manure (FYM), vermicompost, and biofertilizers such as Azotobacter and phosphate solubilizing bacteria.

**2.3 Traits**

Eleven morphological and yield-contributing traits were recorded:

* Days to 50% flowering (DF)
* Days to maturity (DM)
* Plant height (PH, cm)
* Number of primary branches per plant (NPB)
* Number of secondary branches per plant (NSB)
* Number of total branches per plant (NTB)
* Number of seeds per siliqua (NSS)
* Number of siliquae per plant (NSP)
* Harvest index (HI, %)
* Biological yield per plant (BY, g)
* Seed yield per plant (SYP, g)

**2.4 Statistical Analysis**

Genotypic and phenotypic correlation coefficients were computed using the method described by Singh and Chaudhary (1979). The analysis was carried out using R software and Microsoft Excel. Significance of correlation coefficients was tested at both 5% and 1% probability levels. Genotypic correlation coefficients provide insights into genetic relationships, while phenotypic correlations reflect both genetic and environmental influences.

**3. Results and Discussion**

**3.1 Genotypic Correlation Coefficients**

The genotypic correlation analysis revealed significant associations among the traits studied (Table 1). Seed yield per plant (SYP) was positively and significantly correlated with number of seeds per siliqua (NSS) (r = 0.8768\*\*), number of siliquae per plant (NSP) (r = 0.6944\*), and biological yield (BY) (r = 0.6842\*). These findings confirm the importance of these traits as effective selection indices for seed yield improvement in mustard. Plant height (PH) exhibited a highly significant negative correlation with total branches per plant (NTB) (r = -1.070\*\*), indicating that taller plants tend to have fewer branches. This negative association suggests that excessive vegetative growth may limit the development of lateral branches, as also observed by Yadav et al. (2023) and Tripathi et al. (2022). Similarly, days to maturity (DM) was negatively correlated with secondary branches (NSB) (r = -0.795\*\*) and total branches (NTB) (r = -0.755\*\*). A strong positive correlation was observed between secondary branches (NSB) and total branches (NTB) (r = 0.991\*\*), indicating that NSB is a major contributor to overall plant architecture. Moreover, NSP showed a significant positive correlation with SYP, reaffirming its direct influence on seed yield determination.

**3.2 Phenotypic Correlation Coefficients**

Phenotypic correlation coefficients, presented in Table 2, were generally lower in magnitude compared to their genotypic counterparts, reflecting the influence of environmental variation. Nevertheless, SYP retained significant positive correlations with NSS (r = 0.5937\*\*) and NSP (r = 0.5147\*\*), confirming their utility as indirect selection parameters even under variable field conditions. Traits such as days to 50% flowering (DF50) and DM exhibited weak or negative correlations with seed yield, indicating limited direct impact under organic conditions. A significant negative phenotypic correlation was observed between harvest index (HI) and biological yield (BY) (r = -0.5046\*\*), suggesting a trade-off between biomass accumulation and partitioning efficiency.

In present investigation, a narrow difference between the genotypic and phenotypic correlation coefficients was recorded for all the characters. It was found that genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients for almost all the characters studied, indicating presence of strong inherent association among the characters and the environmental effects did not have much influence on these characters. Yield per plant showed highly significant and positive association with number of seeds per siliqua, number of siliqua per plant and biological yield per plant. Similar observations were reported by Ali et al. (2002), Choudhary et al. (2003), Doddabhimappa et al. (2009), Maurya et al. (2012), Rathod et al. (2013), Lodhi et al. (2014), Chauhan et al. (2017), Lyngdoh et al. (2017), Rai et al. (2017), Roy et al. (2017), Prasad and Patil (2018), Tantuway et al. (2018), Singh et al. (2018).

**Table 1: Genotypic correlation coefficient among different traits in mustard genotypes**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Chr** | **DF50** | **DM** | **PH** | **NPB** | **NSB** | **NTB** | **NSS** | **NSP** | **HI** | **BY** | **SYP** |
| **DF50** | 1 \*\* | 0.882 \*\* | 0.5679 | -0.1038 | -0.5346 | -0.4826 | -0.2772 | -0.3791 | -0.0708 | 0.1583 | 0.0484 |
| **DM** |  | 1 \*\* | 0.7569 \*\* | -0.3581 | -0.795 \*\* | -0.755 \*\* | -0.0507 | -0.2949 | -0.0029 | 0.1763 | 0.083 |
| **PH** |  |  | 1 \*\* | -0.957 \*\* | -1.033 \*\* | -1.070 \*\* | -0.0148 | -0.3913 | 0.3535 | 0.117 | 0.2734 |
| **NPB** |  |  |  | 1 \*\* | 0.6785 \* | 0.7706 \*\* | 0.1504 | 0.5877 \* | 0.2845 | -0.1887 | 0.1104 |
| **NSB** |  |  |  |  | 1 \*\* | 0.991 \*\* | 0.102 | 0.2834 | -0.1301 | -0.1923 | -0.1866 |
| **NTB** |  |  |  |  |  | 1 \*\* | 0.1159 | 0.3529 | -0.061 | -0.2012 | -0.1418 |
| **NSS** |  |  |  |  |  |  | 1 \*\* | 0.5064 | 0.1975 | 0.7824 \*\* | 0.8768 \*\* |
| **NSP** |  |  |  |  |  |  |  | 1 \*\* | 0.3075 | 0.4072 | 0.6944 \* |
| **HI** |  |  |  |  |  |  |  |  | 1 \*\* | -0.2928 | 0.4941 |
| **BY** |  |  |  |  |  |  |  |  |  | 1 \*\* | 0.6842 \* |
| **SYP** |  |  |  |  |  |  |  |  |  |  | 1 \*\* |

**Table 2: phenotypic correlation coefficient among different traits in mustard genotype**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Chr** | **DF50** | **DM** | **PH** | **NPB** | **NSB** | **NTB** | **NSS** | **NSP** | **HI** | **BY** | **SYP** |
| **DF50** | 1 \*\* | 0.707 \*\* | 0.1856 | -0.139 | -0.4787 \*\* | -0.445 \*\* | -0.1661 | -0.3197 | 0.0686 | 0.0399 | 0.0662 |
| **DM** |  | 1 \*\* | 0.4833 \*\* | -0.2467 | -0.6827 \*\* | -0.6443 \*\* | -0.0981 | -0.2258 | -0.1119 | 0.2888 | 0.1831 |
| **PH** |  |  | 1 \*\* | -0.3682 \* | -0.5745 \*\* | -0.5738 \*\* | -0.1416 | -0.1456 | -0.0214 | 0.0332 | 0.0132 |
| **NPB** |  |  |  | 1 \*\* | 0.5822 \*\* | 0.7047 \*\* | 0.0217 | 0.4838 \*\* | 0.0595 | 0.0122 | 0.1226 |
| **NSB** |  |  |  |  | 1 \*\* | 0.9871 \*\* | 0.1049 | 0.2996 | -0.0539 | -0.0813 | -0.0881 |
| **NTB** |  |  |  |  |  | 1 \*\* | 0.0958 | 0.3567 \* | -0.0354 | -0.0686 | -0.0528 |
| **NSS** |  |  |  |  |  |  | 1 \*\* | 0.4324 \*\* | 0.3186 | 0.3008 | 0.5937 \*\* |
| **NSP** |  |  |  |  |  |  |  | 1 \*\* | 0.2585 | 0.211 | 0.5147 \*\* |
| **HI** |  |  |  |  |  |  |  |  | 1 \*\* | -0.5046 \*\* | 0.2378 |
| **BY** |  |  |  |  |  |  |  |  |  | 1 \*\* | 0.7107 \*\* |
| SYP |  |  |  |  |  |  |  |  |  |  | 1 \*\* |

**4. Conclusion**

The findings of the study underline the presence of significant genotypic and phenotypic correlations among key yield-contributing traits in mustard genotypes. Seed yield per plant showed strong positive associations with number of seeds per siliqua, siliquae per plant, and biological yield, establishing them as potential selection criteria. The negative associations observed between plant height and branching traits, as well as between harvest index and biological yield, indicate the need for a balanced selection approach. Overall, the results provide a valuable foundation for formulating breeding strategies aimed at enhancing mustard yield under organic farming systems. Future studies should consider multi-location and multi-season trials to validate these trait relationships and improve selection accuracy.

**References**

* Ali N, Farzad J, Jaferieh Y E. and Mýrza M. Y., (2002). Relationship among yield components and selection criteria for yield improvement in winter rapeseed [Brassica napus (L.) Czern. & Coss.]. Pakistan Journal of Botany; 35:167-174.
* Chauhan, JS., Singh, KH., Singh, Manju., Bhadauria, V.P.S. and Kumar, A. (2017). Studies on genetic variability and path analysis for quality characters in Rapeseedmustard (Brassica species). J. Plant Genet. Resour., 21(2):113-117.
* Choudhary, V.K., Kumar, R., Sah, J.N.,(2003). Path analysis in Indian mustard, J App. Biol; 13:6-8.
* Doddabhimappa, R.; Prakash, B. G.; Salimath, P. M.; Ravikumar, R. L. and Rao, M. S. L. (2009). Correlation and path analysis in Indian mustard [Brassica juncea (L.) Czern and Coss]. Karnataka Journal of Agriculture Science. 22(5):971-977
* Lodhi, B., Thakral, N. K., Avtar, A. and Singh, A. (2014). Genetic variability, association and path analysis in Indian mustard (Brassica juncea L.). J. Oilseed Brassica, 2(1):26-31.
* Lyngdoh, Y., Kanaujia, S.P. and Shah, P. (2017). Genetic variability, characters association and path coefficient analysis in green mustard (Brassica juncea L.) genotypes. Int. J. Recent Scientific Res., 8(8)19388-19391.
* Maurya, N.; Singh, A. K. and Singh, S. K. (2012). Inter relationship analysis of yield and yield components in Indian mustard. (Brassica juncea L.). Indian J. Pl. Sci. 1(2-3):90-92.
* Prasad, G., and Patil, BR. (2018). Association and path coefficient analysis in Indian mustard genotypes. Int. J. Chemical Studies, 6(5):362-368.
* Rai, P.K., Ambawat, S., Gurjar, N., Singh, V.V. and Singh, S. (2017). Assessment of genetic variation among drought tolerant recombinant inbred lines (RILs) of Indian mustard (Brassica juncea L.). J. Oilseed Brassica, 8(2):13-150.
* Rathod, V. B., Mehta, D. R. And Solanki, H. V. (2013). Correlation and path coefficient analysis in Indian Mustard [Brassica juncea (L.) Czern & Coss] Agres – An International e-Journal , 2(4): 514-519.
* Roy, R.K., Kumar, A., Kumar, S., Kumar, A. and Kumar, R.R. (2017). Correlation and Path Analysis in Indian Mustard (Brassica juncea L. Czern and Coss) under late sown condition. Environment and Ecology, 36(1A):247-254.
* Singh, R.K. and Chaudhary, B.D. (1979) Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi.
* Singh, S., Dwivedi, A.K., Ashutosh, Meena, O. and Kumar, K. (2018). Genotypic variability, heritability and genetic advance in Indian mustard [Brassica juncea (L.) Czern & Coss.]. Genotypes. J. Pharmacognosy and Phytochemistry, 7(3):350-352.
* Tantuway, G., Srivastava, k., Tirkey, A.,(2018). Character Association and path analysis studies of yield & yield attributing traits in Indian mustard (Brassica juncea ( L.) czern & coss), Plant Archives Vol. 18 ( 2): 2245-2251.
* Warwick, S.I., Francis, A. and J. LaFleche. (2000). Guide to wild germplasm of Brassica and Allied crops (Tribe Brassicaceae).